SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Gonsalves, Dennis
             Pang, Sheng-Zhi

    (ii) TITLE OF INVENTION: TOMATO SPOTTED WILT VIRUS

   (iii) NUMBER OF SEQUENCES: 30

    (iv) CORRESPONDENCE ADDRESS:
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        (E) COUNTRY: U.S.A.
        (F) ZIP: 14603

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/495,484
        (B) FILING DATE: 27-JAN-1994
        (C) CLASSIFICATION:

  (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Goldman, Michael L.
        (B) REGISTRATION NUMBER: 30,727
        (C) REFERENCE/DOCKET NUMBER: 19603/10303

    (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAGGCAAA ACTCGCAGAA CTTGC   25

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCAAGTTCTG CGAGTTTTGC CTGCT					25

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTAACCAT GGTTAAGCTC ACTAAGGAAA GC					32

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCATTCCAT GGTTAACACA CTAAGCAAGC AC					32

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2216 base pairs
        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CAAGTTGAAA GCAACAACAG AACTGTAAAT TCTCTTGCAG TGAAATCTCT GCTCATGTCA      60

GCAGAAAACA ACATCATGCC TAACTCTCAA GCTTCCACTG ATTCTCATTT CAAGCTGAGC     120

CTCTGGCTAA GGGTTCCAAA GGTTTTGAAG CAGGTTTCCA TTCAGAAATT GTTCAAGGTT     180

GCAGGAGATG AAACAAACAA AACATTTTAT TTATCTATTG CCTGCATTCC AAACCATAAC     240

AGTGTTGAGA CAGCTTTAAA CATTACTGTT ATTTGCAAGC ATCAGCTCCC AATTCGCAAA     300

TGCAAAGCTC CTTTTGAATT ATCAATGATG TTTTCTGATT TAAAGGAGCC TTACAACATT     360

GTTCATGACC CTTCATACCC CAAAGGATCG GTTCCAATGC TCTGGCTCGA AACTCACACA     420

TCTTTGCACA AGTTCTTTGC AACTAACTTG CAAGAAGATG TAATCATCTA CACTTTGAAC     480

AACCTTGAGC TAACTCCTGG AAAGTTAGAT TTAGGTGAAA GAACCTTGAA TTACAGTGAA     540

GATGCCTACA AAAGGAAATA TTTCCTTTCA AAAACACTTG AATGTCTTCC ATCTAACACA     600

CAAACTATGT CTTACTTAGA CAGCATCCAA ATCCCTTCAT GGAAGATAGA CTTTGCCAGA     660

GGAGAAATTA AAATTTCTCC ACAATCTATT TCAGTTGCAA AATCTTTGTT AAAGCTTGAT     720

TTAAGCGGGA TCAAAAAGAA AGAATCTAAG GTTAAGGAAG CGTATGCTTC AGGATCAAAA     780

TAATCTTGCT TTGTCCAGCT TTTTCTAATT ATGTTATGTT TATTTTCTTT CTTTACTTAT     840

AATTATTTCT CTGTTTGTCA TCTCTTTCAA ATTCCTCCTG TCTAGTAGAA ACCATAAAAA     900

CAAAAAATAA AAATGAAAAT AAAATTAAAA TAAAATAAAA TCAAAAAATG AAATAAAAAC     960

AACAAAAAAT TAAAAAACGA AAAACCAAAA AGACCCGAAA GGGACCAATT TGGCCAAATT    1020

TGGGTTTTGT TTTTGTTTTT TGTTTTTTGT TTTTTATTTT TTATTTTATT TTTATTTTAT    1080

TTTATTTTTA TTTTATTTTT ATTTTATTTA TTTTTTGTTT TCGTTGTTTT TGTTATTTTA    1140

TTATTTATTA AGCACAACAC ACAGAAAGCA AACTTTAATT AAACACACTT ATTTAAAATT    1200

TAACACACTA AGCAAGCACA AGCAATAAAG ATAAAGAAAG CTTTATATAT TTATAGGCTT    1260

TTTTATAATT TAACTTACAG CTGCTTTCAA GCAAGTTCTG CGAGTTTTGC CTGCTTTTTA    1320

ACCCCGAACA TTTCATAGAA CTTGTTAAGA GTTTCACTGT AATGTTCCAT AGCAACACTC    1380

CCTTTAGCAT TAGGATTGCT GGAGCTAAGT ATAGCAGCAT ACTCTTTCCC CTTCTTCACC    1440
```

```
TGATCTTCAT TCATTTCAAA TGCTTTGCTT TTCAGCACAG TGCAAACTTT TCCTAAGGCT      1500

TCCTTGGTGT CATACTTCTT TGGGTCGATC CCGAGGTCCT TGTATTTTGC ATCCTGATAT      1560

ATAGCCAAGA CAACACTGAT CATCTCAAAG CTATCAACTG AAGCAATAAG AGGTAAGCTA      1620

CCTCCCAGCA TTATGGCAAG TCTCACAGAC TTTGCATCAT CGAGAGGTAA TCCATAGGCT      1680

TGAATCAAAG GATGGGAAGC AATCTTAGAT TTGATAGTAT TGAGATTCTC AGAATTCCCA      1740

GTTTCTTCAA CAAGCCTGAC CCTGATCAAG CTATCAAGCC TTCTGAAGGT CATGTCAGTG      1800

CCTCCAATCC TGTCTGAAGT TTTCTTTATG GTAATTTTAC CAAAAGTAAA ATCGCTTTGC      1860

TTAATAACCT TCATTATGCT CTGACGATTC TTTAGGAATG TCAGACATGA AATAACGCTC      1920

ATCTTCTTGA TCTGGTCGAT GTTTTCCAGA CAAAAAGTCT TGAAGTTGAA TGCTACCAGA      1980

TTCTGATCTT CCTCAAACTC AAGGTCTTTG CCTTGTGTCA ACAAAGCAAC AATGCTTTCC      2040

TTAGTGAGCT TAACCTTAGA CATGATGATC GTAAAAGTTG TTATATGCTT TGACCGTATG      2100

TAACTCAAGG TGCGAAAGTG CAACTCTGTA TCCCGCAGTC GTTTCTTAGG TTCTTAATGT      2160

GATGATTTGT AAGACTGAGT GTTAAGGTAT GAACACAAAA TTGACACGAT TGCTCT         2216
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1709 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
AAATTCTCTT GCAGTGAAAT CTCTGCTCAT GTTAGCAGAA AACAACATCA TGCCTAACTC        60

TCAAGCTTTT GTCAAAGCTT CTACTGATTC TAATTTCAAG CTGAGCCTCT GGCTAAGGGT       120

TCCAAAGGTT TTGAAGCAGA TTTCCATTCA GAAATTGTTC AAGGTTGCAG GAGATGAAAC       180

AAATAAAACA TTTTATTTAT CTATTGCCTG CATTCCAAAC CATAACAGTG TTGAGACAGC       240

TTTAAACATT ACTGTTATTT GCAAGCATCA GCTCCCAATT CGTAAATGTA AAACTCCTTT       300

TGAATTATCA ATGATGTTTT CTGATTTAAA GGAGCCTTAC AACATTATTC ATGATCCTTC       360

ATATCCCCAA AGGATTGTTC ATGCTCTGCT TGAAACTCAC ACATCTTTTG CACAAGTTCT       420
```

```
TTGCAACAAC TTGCAAGAAG ATGTGATCAT CTACACCTTG AACAACCATG AGCTAACTCC        480

TGGAAAGTTA GATTTAGGTG AAATAACTTT GAATTACAAT GAAGACGCCT ACAAAAGGAA        540

ATATTTCCTT TCAAAAACAC TTGAATGTCT TCCATCTAAC ATACAAACTA TGTCTTATTT        600

AGACAGCATC CAAATCCCTT CCTGGAAGAT AGACTTTGCC AGGGGAGAAA TTAAAATTTC        660

TCCACAATCT ATTTCAGTTG CAAATCTTT GTTAAATCTT GATTTAAGCG GGATTAAAAA        720

GAAAGAATCT AAGATTAAGG AAGCATATGC TTCAGGATCA AAATGATCTT GCTGTGTCCA        780

GCTTTTTCTA ATTATGTTAT GTTATTTTC TTTCTTTACT TATAATTATT TTTCTGTTTG        840

TCATTTCTTT CAAATTCCTC CTGTCTAGTA GAAACCATAA AAACAAAAT AAAAATAAAA        900

TAAAATCAAA ATAAAATAAA AATCAAAAAA TGAAATAAAA GCAACAAAAA AATTAAAAAA        960

CAAAAAACCA AAAAGATCC CGAAAGGACA ATTTTGGCCA AATTTGGGGT TTGTTTTTGT       1020

TTTTTGTTTT TTTGTTTTTT GTTTTTATTT TTATTTTTAT TTTTATTTTT ATTTTATTTT       1080

ATTTTATGTT TTTGTTGTTT TTGTTATTTT GTTATTTATT AAGCACAACA CACAGAAAGC       1140

AAACTTTAAT TAAACACACT TATTTAAAAT TTAACACACT AAGCAAGCAC AAACAATAAA       1200

GATAAAGAAA GCTTTATATA TTTATAGGCT TTTTTATAAT TTAACTTACA GCTGCTTTTA       1260

AGCAAGTTCT GTGAGTTTTG CCTGTTTTTT AACCCCAAAC ATTTCATAGA ACTTGTTAAG       1320

GGTTTCACTG TAATGTTCCA TAGCAATACT TCCTTTAGCA TTAGGATTGC TGGAGCTAAG       1380

TATAGCAGCA TACTCTTTCC CCTTCTTCAC CTGATCTTCA TTCATTTCAA ATGCTTTTCT       1440

TTTCAGCACA GTGCAAACTT TTCCTAAGGC TTCCCTGGTG TCATACTTCT TTGGGTCGAT       1500

CCCGAGATCC TTGTATTTTG CATCCTGATA TATAGCCAAG ACAACACTGA TCATCTCAAA       1560

GCTATCAACT GAAGCAATAA GAGGTAAGCT ACCTCCCAGC ATTATGGCAA GCCTCACAGA       1620

CTTTGCATCA TCAAGAGGTA ATCCATAGGC TTGAATCAAA GGGTGGGAAG CAATCTTAGA       1680

TTTGATAGTA TTGAGATTCT CAGAATTCC                                       1709
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 260 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Gln Val Glu Ser Asn Asn Arg Thr Val Asn Ser Leu Ala Val Lys Ser
1               5                   10              15
```

```
Leu Leu Met Ser Ala Glu Asn Asn Ile Met Pro Asn Ser Gln Ala Ser
            20              25              30
```

```
Thr Asp Ser His Phe Lys Leu Ser Leu Trp Leu Arg Val Pro Lys Val
        35              40              45
```

```
Leu Lys Gln Val Ser Ile Gln Lys Leu Phe Lys Val Ala Gly Asp Glu
    50              55              60
```

```
Thr Asn Lys Thr Phe Tyr Leu Ser Ile Ala Cys Ile Pro Asn His Asn
65              70              75                      80
```

```
Ser Val Glu Thr Ala Leu Asn Ile Thr Val Ile Cys Lys His Gln Leu
            85              90              95
```

```
Pro Ile Arg Lys Cys Lys Ala Pro Phe Glu Leu Ser Met Met Phe Ser
            100             105             110
```

```
Asp Leu Lys Glu Pro Tyr Asn Ile Val His Asp Pro Ser Tyr Pro Lys
        115             120             125
```

```
Gly Ser Val Pro Met Leu Trp Leu Glu Thr His Thr Ser Leu His Lys
    130             135             140
```

```
Phe Phe Ala Thr Asn Leu Gln Glu Asp Val Ile Ile Tyr Thr Leu Asn
145             150             155             160
```

```
Asn Leu Glu Leu Thr Pro Gly Lys Leu Asp Leu Gly Glu Arg Thr Leu
            165             170             175
```

```
Asn Tyr Ser Glu Asp Ala Tyr Lys Arg Lys Tyr Phe Leu Ser Lys Thr
        180             185             190
```

```
Leu Glu Cys Leu Pro Ser Asn Thr Gln Thr Met Ser Tyr Leu Asp Ser
        195             200             205
```

```
Ile Gln Ile Pro Ser Trp Lys Ile Asp Phe Ala Arg Gly Glu Ile Lys
    210             215             220
```

```
Ile Ser Pro Gln Ser Ile Ser Val Ala Lys Ser Leu Leu Lys Leu Asp
225             230             235             240
```

```
Leu Ser Gly Ile Lys Lys Lys Glu Ser Lys Val Lys Glu Ala Tyr Ala
            245             250             255
```

```
Ser Gly Ser Lys
            260
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 858 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTAACACACT AAGCAAGCAC AAACAATAAA GATAAAGAAA GCTTTATATA TTTATAGGCT   60

TTTTTATAAT TTAACTTACA GCTGCTTTTA AGCAAGTTCT GTGAGTTTTG CCTGTTTTTT   120

AACCCCAAAC ATTTCATAGA ACTTGTTAAG GGTTTCACTG TAATGTTCCA TAGCAATACT   180

TCCTTTAGCA TTAGGATTGC TGGAGCTAAG TATAGCAGCA TACTCTTTCC CCTTCTTCAC   240

CTGATCTTCA TTCATTTCAA ATGCTTTTCT TTTCAGCACA GTGCAAACTT TTCCTAAGGC   300

TTCCCTGGTG TCATACTTCT TTGGGTCGAT CCCGAGATCC TTGTATTTTG CATCCTGATA   360

TATAGCCAAG ACAACACTGA TCATCTCAAA GCTATCAACT GAAGCAATAA GAGGTAAGCT   420

ACCTCCCAGC ATTATGGCAA GCCTCACAGA CTTTGCATCA TCAAGAGGTA ATCCATAGGC   480

TTGACTCAAA GGGTGGGAAG CAATCTTAGA TTTGATAGTA TTGAGATTCT CAGAATTCCC   540

AGTTTCCTCA ACAAGCCTGA CCCTGATCAA GCTATCAAGC CTTCTGAAGG TCATGTCAGT   600

GGCTCCAATC CTGTCTGAAG TTTTCTTTAT GGTAATTTTA CCAAAAGTAA AATCGCTTTG   660

CTTAATAACC TTCATTATGC TCTGACGATT CTTCAGGAAT GTCAGACATG AAATAATGCT   720

CATCTTTTTG ATCTGGTCAA GGTTTTCCAG ACAAAAAGTC TTGAAGTTGA ATGCTACCAG   780

ATTCTGATCT TCCTCAAACT CAAGGTCTTT GCCTTGTGTC AACAAAGCAA CAATGCTTTC   840

CTTAGTGAGC TTAACCAT   858

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2028 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
AAATTCTCTT GCAGTGAAAT CTCTGCTCAT GTTAGCAGAA AACAACATCA TGCCTAACTC        60

TCAAGCTTTT GTCAAAGCTT CTACTGATTC TAATTTCAAG CTGAGCCTCT GGCTAAGGGT       120

TCCAAAGGTT TTGAAGCAGA TTTCCATTCA GAAATTGTTC AAGGTTGCAG GAGATGAAAC       180

AAATAAAACA TTTTATTTAT CTATTGCCTG CATTCCAAAC CATAACAGTG TTGAGACAGC       240

TTTAAACATT ACTGTTATTT GCAAGCATCA GCTCCCAATT CGTAAATGTA AAACTCCTTT       300

TGAATTATCA ATGATGTTTT CTGATTTAAA GGAGCCTTAC AACATTATTC ATGATCCTTC       360

ATATCCCCAA AGGATTGTTC ATGCTCTGCT TGAAACTCAC ACATCTTTTG CACAAGTTCT       420

TTGCAACAAC TTGCAAGAAG ATGTGATCAT CTACACCTTG AACAACCATG AGCTAACTCC       480

TGGAAAGTTA GATTTAGGTG AAATAACTTT GAATTACAAT GAAGACGCCT ACAAAAGGAA       540

ATATTTCCTT TCAAAAACAC TTGAATGTCT TCCATCTAAC ATACAAACTA TGTCTTATTT       600

AGACAGCATC CAAATCCCTT CCTGGAAGAT AGACTTTGCC AGGGGAGAAA TTAAAATTTC       660

TCCACAATCT ATTTCAGTTG CAAATCTTT GTTAAATCTT GATTTAAGCG GGATTAAAAA       720

GAAAGAATCT AAGATTAAGG AAGCATATGC TTCAGGATCA AAATGATCTT GCTGTGTCCA       780,

GCTTTTTCTA ATTATGTTAT GTTTATTTTC TTTCTTTACT TATAATTATT TTTCTGTTTG       840

TCATTTCTTT CAAATTCCTC CTGTCTAGTA GAAACCATAA AAACAAAAAT AAAAATAAAA       900

TAAAATCAAA ATAAAATAAA AATCAAAAAA TGAAATAAAA GCAACAAAAA AATTAAAAAA       960

CAAAAAACCA AAAAAGATCC CGAAAGGACA ATTTTGGCCA AATTTGGGGT TTGTTTTTGT      1020

TTTTTGTTTT TTTGTTTTTT GTTTTTATTT TTATTTTTAT TTTTATTTTT ATTTTATTTT      1080

ATTTTATGTT TTTGTTGTTT TTGTTATTTT GTTATTTATT AAGCACAACA CACAGAAAGC      1140

AAACTTTAAT TAAACACACT TATTTAAAAT TTAACACACT AAGCAAGCAC AAACAATAAA      1200

GATAAAGAAA GCTTTATATA TTTATAGGCT TTTTTATAAT TTAACTTACA GCTGCTTTTA      1260

AGCAAGTTCT GTGAGTTTTG CCTGTTTTTT AACCCCAAAC ATTTCATAGA ACTTGTTAAG      1320

GGTTTCACTG TAATGTTCCA TAGCAATACT TCCTTTAGCA TTAGGATTGC TGGAGCTAAG      1380

TATAGCAGCA TACTCTTTCC CCTTCTTCAC CTGATCTTCA TTCATTTCAA ATGCTTTTCT      1440

TTTCAGCACA GTGCAAACTT TTCCTAAGGC TTCCCTGGTG TCATACTTCT TTGGGTCGAT      1500

CCCGAGATCC TTGTATTTTG CATCCTGATA TATAGCCAAG ACAACACTGA TCATCTCAAA      1560

GCTATCAACT GAAGCAATAA GAGGTAAGCT ACCTCCCAGC ATTATGGCAA GCCTCACAGA      1620
```

CTTTGCATCA TCAAGAGGTA ATCCATAGGC TTGACTCAAA GGGTGGGAAG CAATCTTAGA   1680

TTTGATAGTA TTGAGATTCT CAGAATTCCC AGTTTCCTCA ACAAGCCTGA CCCTGATCAA   1740

GCTATCAAGC CTTCTGAAGG TCATGTCAGT GGCTCCAATC CTGTCTGAAG TTTTCTTTAT   1800

GGTAATTTTA CCAAAAGTAA AATCGCTTTG CTTAATAACC TTCATTATGC TCTGACGATT   1860

CTTCAGGAAT GTCAGACATG AAATAATGCT CATCTTTTTG ATCTGGTCAA GGTTTTCCAG   1920

ACAAAAAGTC TTGAAGTTGA ATGCTACCAG ATTCTGATCT TCCTCAAACT CAAGGTCTTT   1980

GCCTTGTGTC AACAAAGCAA CAATGCTTTC CTTAGTGAGC TTAACCAT   2028

(2) INFORMATION FOR SEQ ID NO:10:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 21 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTGGTCTT CTTCAAACTC A   21

(2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 18 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGTAGCCAT GAGCAAAG   18

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 467 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Met Ser Ser Gly Val Tyr Glu Ser Ile Ile Gln Thr Lys Ala Ser Val
1               5                   10              15

Trp Gly Ser Thr Ala Ser Gly Lys Ser Ile Val Asp Ser Tyr Trp Ile
            20                  25                  30

Tyr Glu Phe Pro Thr Gly Ser Pro Leu Val Gln Thr Gln Leu Tyr Ser
        35                  40                  45

Asp Ser Arg Ser Lys Ser Ser Phe Gly Tyr Thr Ser Lys Ile Gly Asp
    50                  55                  60

Ile Pro Ala Val Glu Glu Glu Ile Leu Ser Gln Asn Val His Ile Pro
65              70                  75                      80

Val Phe Asp Asp Ile Asp Phe Ser Ile Asn Ile Asn Asp Ser Phe Leu
            85                  90                  95

Ala Ile Ser Val Cys Ser Asn Thr Val Asn Thr Asn Gly Val Lys His
            100                 105                 110

Gln Gly His Leu Lys Val Leu Ser Leu Ala Gln Leu His Pro Phe Glu
        115                 120                 125

Pro Val Met Ser Arg Ser Glu Ile Ala Ser Arg Phe Arg Leu Gln Glu
    130                 135                 140

Glu Asp Ile Ile Pro Asp Asp Lys Tyr Ile Ser Ala Ala Asn Lys Gly
145                 150                 155                 160

Ser Leu Ser Cys Val Lys Glu His Thr Tyr Lys Val Glu Met Ser His
            165                 170                 175

Asn Gln Ala Leu Gly Lys Val Asn Val Leu Ser Pro Asn Arg Asn Val
        180                 185                 190

His Glu Trp Leu Tyr Ser Phe Lys Pro Asn Phe Asn Gln Ile Glu Ser
        195                 200                 205

Asn Asn Arg Thr Val Asn Ser Leu Ala Val Lys Ser Leu Leu Met Ala
    210                 215                 220

Thr Glu Asn Asn Ile Met Pro Asn Ser Gln Ala Phe Val Lys Ala Ser
225                 230                 235                 240

Thr Asp Ser His Phe Lys Leu Ser Leu Trp Leu Arg Ile Pro Lys Val
            245                 250                 255

Leu Lys Gln Ile Ala Ile Gln Lys Leu Phe Lys Phe Ala Gly Asp Glu
```

```
                    260                      265                      270
   Thr Gly Lys Ser Phe Tyr Leu Ser Ile Ala Cys Ile Pro Asn His Asn
           275                      280                  285

   Ser Val Glu Thr Ala Leu Asn Val Thr Val Ile Cys Arg His Gln Leu
           290                      295                  300

   Pro Ile Pro Lys Ser Lys Ala Pro Phe Glu Leu Ser Met Ile Phe Ser
   305                      310                      315                 320

   Asp Leu Lys Glu Pro Tyr Asn Thr Val His Asp Pro Ser Tyr Pro Gln
                       325                      330                  335

   Arg Ile Val His Ala Leu Leu Glu Thr His Thr Ser Phe Ala Gln Val
                   340                      345                  350

   Leu Cys Asn Lys Leu Gln Glu Asp Val Ile Ile Tyr Thr Ile Asn Ser
               355                      360                  365

   Pro Glu Leu Thr Pro Ala Lys Leu Asp Leu Gly Glu Arg Thr Leu Asn
           370                      375                  380

   Tyr Ser Glu Asp Ala Ser Lys Lys Lys Tyr Phe Leu Ser Lys Thr Leu
   385                      390                      395                 400

   Glu Cys Leu Pro Val Asn Val Gln Thr Met Ser Tyr Leu Asp Ser Ile
                   405                      410                  415

   Gln Ile Pro Ser Trp Lys Ile Asp Phe Ala Arg Gly Glu Ile Arg Ile
                   420                      425                  430

   Ser Pro Gln Ser Thr Pro Ile Ala Arg Ser Leu Leu Lys Leu Asp Leu
           435                      440                  445

   Ser Lys Ile Lys Glu Lys Lys Ser Leu Thr Trp Glu Thr Ser Ser Tyr
           450                      455                  460

   Asp Leu Glu
   465
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 258 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ser	Lys	Val	Lys	Leu	Thr	Lys	Glu	Asn	Ile	Val	Ser	Leu	Leu	Thr
1				5					10					15	

Gln	Ser	Ala	Asp	Val	Glu	Phe	Glu	Glu	Asp	Gln	Asn	Gln	Val	Ala	Phe
			20					25					30		

Asn	Phe	Lys	Thr	Phe	Cys	Gln	Glu	Asn	Leu	Asp	Leu	Ile	Lys	Lys	Met
		35					40					45			

Ser	Ile	Thr	Ser	Cys	Leu	Thr	Phe	Leu	Lys	Asn	Arg	Gln	Gly	Ile	Met
	50					55					60				

Lys	Val	Val	Asn	Gln	Ser	Asp	Phe	Thr	Phe	Gly	Lys	Val	Thr	Ile	Lys
65					70					75					80

Lys	Asn	Ser	Glu	Arg	Val	Gly	Ala	Lys	Asp	Met	Thr	Phe	Arg	Arg	Leu
				85					90					95	

Asp	Ser	Met	Ile	Arg	Val	Lys	Leu	Ile	Glu	Glu	Thr	Ala	Asn	Asn	Glu
			100					105					110		

Asn	Leu	Ala	Ile	Ile	Lys	Ala	Lys	Ile	Ala	Ser	His	Pro	Leu	Val	Gln
		115					120					125			

Ala	Tyr	Gly	Leu	Pro	Leu	Ala	Asp	Ala	Lys	Ser	Val	Arg	Leu	Ala	Ile
	130					135					140				

Met	Leu	Gly	Gly	Ser	Ile	Pro	Leu	Ile	Ala	Ser	Val	Asp	Ser	Phe	Glu
145					150					155					160

Met	Ile	Ser	Val	Val	Leu	Ala	Ile	Tyr	Gln	Asp	Ala	Lys	Tyr	Lys	Glu
				165					170					175	

Leu	Gly	Ile	Glu	Pro	Thr	Lys	Tyr	Asn	Thr	Lys	Glu	Ala	Leu	Gly	Lys
			180					185					190		

Val	Cys	Thr	Val	Leu	Lys	Ser	Lys	Gly	Phe	Thr	Met	Asp	Asp	Ala	Gln
		195					200					205			

Ile	Asn	Lys	Gly	Lys	Glu	Tyr	Ala	Lys	Ile	Leu	Ser	Ser	Cys	Asn	Pro
	210					215					220				

Asn	Ala	Lys	Gly	Ser	Ile	Ala	Met	Asp	Tyr	Tyr	Ser	Asp	Asn	Leu	Asp
225					230					235					240

Lys	Phe	Tyr	Glu	Met	Phe	Gly	Val	Lys	Lys	Glu	Ala	Lys	Ile	Ala	Gly
				245					250					255	

Val	Ala

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 3049 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGAGCAATTG GGTCATTTTT TATTCTAAAT CGAACCTCAA CTAGCAAATC TCAGAACTGT   60

AATAAGCACA AGAGCACAAG AGCCACAATG TCATCAGGTG TTTATGAATC GATCATTCAG   120

ACAAAGGCTT CAGTTTGGGG ATCGACAGCA TCTGGTAAGT CCATCGTGGA TTCTTACTGG   180

ATTTATGAGT TTCCAACTGG TTCTCCACTG GTTCAAACTC AGTTGTACTC TGATTCGAGG   240

AGCAAAAGTA GCTTCGGCTA CACTTCAAAA ATTGGTGATA TTCCTGCTGT AGAGGAGGAA   300

ATTTTATCTC AGAACGTTCA TATCCCAGTG TTTGATGATA TTGATTTCAG CATCAATATC   360

AATGATTCTT TCTTGGCAAT TTCTGTTTGT TCCAACACAG TTAACACCAA TGGAGTGAAG   420

CATCAGGGTC ATCTTAAAGT TCTTTCTCTT GCCCAATTGC ATCCCTTTGA ACCTGTGATG   480

AGCAGGTCAG AGATTGCTAG CAGATTCCGG CTCCAAGAAG AAGATATAAT TCCTGATGAC   540

AAATATATAT CTGCTGCTAA CAAGGGATCT CTCTCCTGTG TCAAAGAACA TACTTACAAA   600

GTCGAAATGA GCCACAATCA GGCTTTAGGC AAAGTGAATG TTCTTTCTCC TAACAGAAAT   660

GTTCATGAGT GGCTGTATAG TTTCAAACCA AATTTCAACC AGATCGAAAG TAATAACAGA   720

ACTGTAAATT CTCTTGCAGT CAAATCTTTG CTCATGGCTA CAGAAAACAA CATTATGCCT   780

AACTCTCAAG CTTTTGTTAA AGCTTCTACT GATTCTCATT TTAAGTTGAG CCTTTGGCTG   840

AGAATTCCAA AAGTTTTGAA GCAAATAGCC ATACAGAAGC TCTTCAAGTT TGCAGGAGAC   900

GAAACCGGTA AAAGTTTCTA TTTGTCTATT GCATGCATCC CAAATCACAA CAGTGTGGAA   960

ACAGCTTTAA ATGTCACTGT TATATGTAGA CATCAGCTTC CAATCCCTAA GTCCAAAGCT   1020

CCTTTTGAAT TATCAATGAT TTTCTCCGAT CTGAAAGAGC CTTACAACAC TGTGCATGAT   1080

CCTTCATATC CTCAAAGGAT TGTTCATGCT TTGCTTGAGA CTCACACTTC CTTTGCACAA   1140

GTTCTCTGCA ACAAGCTGCA AGAAGATGTG ATCATATATA CTATAAACAG CCCTGAACTA   1200

ACCCCAGCTA AGCTGGATCT AGGTGAAAGA ACCTTGAACT ACAGTGAAGA TGCTTCGAAG   1260

AAGAAGTATT TTCTTTCAAA AACACTCGAA TGCTTGCCAG TAAATGTGCA GACTATGTCT   1320

TATTTGGATA GCATCCAGAT TCCTTCATGG AAGATAGACT TTGCCAGAGG AGAGATCAGA   1380

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ATCTCCCCTC AATCTACTCC TATTGCAAGA TCTTTGCTCA AGCTGGATTT GAGCAAGATC     1440

AAGGAAAAGA AGTCCTTGAC TTGGGAAACA TCCAGCTATG ATCTAGAATA AAAGTGGCTC     1500

ATACTACTCT AAGTAGTATT TGTCAACTTG CTTATCCTTT ATGTTGTTTA TTTCTTTTAA     1560

ATCTAAAGTA AGTTAGATTC AAGTAGTTTA GTATGCTATA GCATTATTAC AAAAAATACA     1620

AAAAAATACA AAAAAATACA AAAAATATAA AAAACCCAAA AAGATCCCAA AAGGGACGAT     1680

TTGGTTGATT TACTCTGTTT TAGGCTTATC TAAGCTGCTT TTGTTTGAGC AAAATAACAT     1740

TGTAACATGC AATAACTGGA ATTTAAAGTC CTAAAGAAG TTTCAAAGGA CAGCTTAGCC     1800

AAAATTGGTT TTTGTTTTTG TTTTTTTGTT TTTTGTTTTT TTGTTTTATT TTTATTTTTA     1860

GTTTATTTTT TGTTTTTGTT ATTTTTATTT TTATTTTATT TTCTTTTATT TTATTTATAT     1920

ATATATCAAA CACAATCCAC ACAAATAATT TTAATTTCAA ACATTCTACT GATTTAACAC     1980

ACTTAGCCTG ACTTTATCAC ACTTAACACG CTTAGTTAGG CTTTAACACA CTGAACTGAA     2040

TTAAAACACA CTTAGTATTA TGCATCTCTT AATTAACACA CTTTAATAAT ATGCATCTCT     2100

GAATCAGCCT TAAAGAAGCT TTTATGCAAC ACCAGCAATC TTGGCCTCTT TCTTAACTCC     2160

AAACATTTCA TAGAATTTGT CAAGATTATC ACTGTAATAG TCCATAGCAA TGCTTCCCTT     2220

AGCATTGGGA TTGCAAGAAC TAAGTATCTT GGCATATTCT TTCCCTTTGT TTATCTGTGC     2280

ATCATCCATT GTAAATCCTT TGCTTTTAAG CACTGTGCAA ACCTTCCCCA GAGCTTCCTT     2340

AGTGTTGTAC TTAGTTGGTT CAATCCCTAA CTCCTTGTAC TTTGCATCTT GATATATGGC     2400

AAGAACAACA CTGATCATCT CGAAGCTGTC AACAGAAGCA ATGAGAGGGA TACTACCTCC     2460

AAGCATTATA GCAAGTCTCA CAGATTTTGC ATCTGCCAGA GGCAGCCCGT AAGCTTGGAC     2520

CAAAGGGTGG GAGGCAATTT TTGCTTTGAT AATAGCAAGA TTCTCATTGT TTGCAGTCTC     2580

TTCTATGAGC TTCACTCTTA TCATGCTATC AAGCCTCCTG AAAGTCATAT CCTTAGCTCC     2640

AACTCTTTCA GAATTTTTCT TTATCGTGAC CTTACCAAAA GTAAAATCAC TTTGGTTCAC     2700

AACTTTCATA ATGCCTTGGC GATTCTTCAA GAAAGTCAAA CATGAAGTGA TACTCATTTT     2760

CTTAATCAGG TCAAGATTTT CCTGACAGAA AGTCTTAAAG TTGAATGCGA CCTGGTTCTG     2820

GTCTTCTTCA AACTCAACAT CTGCAGATTG AGTTAAAAGA GAGACAATGT TTTCTTTTGT     2880

GAGCTTGACC TTAGACATGG TGGCAGTTTA GATCTAGACC TTTCTCGAGA GATAAGATTC     2940

AAGGTGAGAA AGTGCAACAC TGTAGACCGC GGTCGTTACT TATCCTGTTA ATGTGATGAT     3000
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TTGTATTGCT GAGTATTAGG TTTTTGAATA AAATTGACAC AATTGCTCT   3049

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 777 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTATGCAACA CCAGCAATCT TGGCCTCTTT CTTAACTCCA AACATTTCAT AGAATTTGTC   60

AAGATTATCA CTGTAATAGT CCATAGCAAT GCTTCCCTTA GCATTGGGAT TGCAAGAACT   120

AAGTATCTTG GCATATTCTT TCCCTTTGTT TATCTGTGCA TCATCCATTG TAAATCCTTT   180

GCTTTTAAGC ACTGTGCAAA CCTTCCCCAG AGCTTCCTTA GTGTTGTACT TAGTTGGTTC   240

AATCCCTAAC TCCTTGTACT TTGCATCTTG ATATATGGCA AGAACAACAC TGATCATCTC   300

GAAGCTGTCA ACAGAAGCAA TGAGAGGGAT ACTACCTCCA AGCATTATAG CAAGTCTCAC   360

AGATTTTGCA TCTGCCAGAG GCAGCCCGTA AGCTTGGACC AAAGGGTGGG AGGCAATTTT   420

TGCTTTGATA ATAGCAAGAT TCTCATTGTT TGCAGTCTCT TCTATGAGCT TCACTCTTAT   480

CATGCTATCA AGCCTCCTGA AAGTCATATC CTTAGCTCCA ACTCTTTCAG AATTTTTCTT   540

TATCGTGACC TTACCAAAAG TAAAATCACT TTGGTTCACA ACTTTCATAA TGCCTTGGCG   600

ATTCTTCAAG AAAGTCAAAC ATGAAGTGAT ACTCATTTTC TTAATCAGGT CAAGATTTTC   660

CTGACAGAAA GTCTTAAAGT TGAATGCGAC CTGGTTCTGG TCTTCTTCAA ACTCAACATC   720

TGCAGATTGA GTTAAAAGAG AGACAATGTT TTCTTTTGTG AGCTTGACCT TAGACAT   777

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTCTGAGAT TTGCTAGT   18

(2) INFORMATION FOR SEQ ID NO:17:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 18 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTATATCTTC TTCTTGGA   18

(2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1401 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGTCATCAG GTGTTTATGA ATCGATCATT CAGACAAAGG CTTCAGTTTG GGGATCGACA   60

GCATCTGGTA AGTCCATCGT GGATTCTTAC TGGATTTATG AGTTTCCAAC TGGTTCTCCA   120

CTGGTTCAAA CTCAGTTGTA CTCTGATTCG AGGAGCAAAA GTAGCTTCGG CTACACTTCA   180

AAAATTGGTG ATATTCCTGC TGTAGAGGAG GAAATTTTAT CTCAGAACGT TCATATCCCA   240

GTGTTTGATG ATATTGATTT CAGCATCAAT ATCAATGATT CTTTCTTGGC AATTTCTGTT   300

TGTTCCAACA CAGTTAACAC CAATGGAGTG AAGCATCAGG GTCATCTTAA AGTTCTTTCT   360

CTTGCCCAAT TGCATCCCTT TGAACCTGTG ATGAGCAGGT CAGAGATTGC TAGCAGATTC   420

CGGCTCCAAG AAGAAGATAT AATTCCTGAT GACAAATATA TATCTGCTGC TAACAAGGGA   480

TCTCTCTCCT GTGTCAAAGA ACATACTTAC AAAGTCGAAA TGAGCCACAA TCAGGCTTTA   540

GGCAAAGTGA ATGTTCTTTC TCCTAACAGA AATGTTCATG AGTGGCTGTA TAGTTTCAAA   600

CCAAATTTCA ACCAGATCGA AAGTAATAAC AGAACTGTAA ATTCTCTTGC AGTCAAATCT   660

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TTGCTCATGG CTACAGAAAA CAACATTATG CCTAACTCTC AAGCTTTTGT TAAAGCTTCT      720

ACTGATTCTC ATTTTAAGTT GAGCCTTTGG CTGAGAATTC CAAAAGTTTT GAAGCAAATA      780

GCCATACAGA AGCTCTTCAA GTTTGCAGGA GACGAAACCG GTAAAAGTTT CTATTTGTCT      840

ATTGCATGCA TCCCAAATCA CAACAGTGTG GAAACAGCTT TAAATGTCAC TGTTATATGT      900

AGACATCAGC TTCCAATCCC TAAGTCCAAA GCTCCTTTTG AATTATCAAT GATTTTCTCC      960

GATCTGAAAG AGCCTTACAA CACTGTGCAT GATCCTTCAT ATCCTCAAAG GATTGTTCAT     1020

GCTTTGCTTG AGACTCACAC TTCCTTTGCA CAAGTTCTCT GCAACAAGCT GCAAGAAGAT     1080

GTGATCATAT ATACTATAAA CAGCCCTGAA CTAACCCCAG CTAAGCTGGA TCTAGGTGAA     1140

AGAACCTTGA ACTACAGTGA AGATGCTTCG AAGAAGAAGT ATTTTCTTTC AAAAACACTC     1200

GAATGCTTGC CAGTAAATGT GCAGACTATG TCTTATTTGG ATAGCATCCA GATTCCTTCA     1260

TGGAAGATAG ACTTTGCCAG AGGAGAGATC AGAATCTCCC CTCAATCTAC TCCTATTGCA     1320

AGATCTTTGC TCAAGCTGGA TTTGAGCAAG ATCAAGGAAA AGAAGTCCTT GACTTGGGAA     1380

ACATCCAGCT ATGATCTAGA A                                              1401
```

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 777 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATGTCTAAGG TCAAGCTCAC AAAAGAAAC ATTGTCTCTC TTTTAACTCA ATCTGCAGAT       60

GTTGAGTTTG AAGAAGACCA GAACCAGGTC GCATTCAACT TTAAGACTTT CTGTCAGGAA      120

AATCTTGACC TGATTAAGAA AATGAGTATC ACTTCATGTT TGACTTTCTT GAAGAATCGC      180

CAAGGCATTA TGAAAGTTGT GAACCAAAGT GATTTTACTT TTGGTAAGGT CACGATAAAG      240

AAAAATTCTG AAAGAGTTGG AGCTAAGGAT ATGACTTTCA GGAGGCTTGA TAGCATGATA      300

AGAGTGAAGC TCATAGAAGA GACTGCAAAC AATGAGAATC TTGCTATTAT CAAAGCAAAA      360

ATTGCCTCCC ACCCTTTGGT CCAAGCTTAC GGGCTGCCTC TGGCAGATGC AAAATCTGTG      420

AGACTTGCTA TAATGCTTGG AGGTAGTATC CCTCTCATTG CTTCTGTTGA CAGCTTCGAG      480
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ATGATCAGTG TTGTTCTTGC CATATATCAA GATGCAAAGT ACAAGGAGTT AGGGATTGAA        540

CCAACTAAGT ACAACACTAA GGAAGCTCTG GGGAAGGTTT GCACAGTGCT TAAAAGCAAA        600

GGATTTACAA TGGATGATGC ACAGATAAAC AAAGGGAAAG AATATGCCAA GATACTTAGT        660

TCTTGCAATC CCAATGCTAA GGGAAGCATT GCTATGGACT ATTACAGTGA TAATCTTGAC        720

AAATTCTATG AAATGTTTGG AGTTAAGAAA GAGGCCAAGA TTGCTGGTGT TGCATAA           777
```

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
TACTTATCTA GAACCATGGA CAAAGCAAAG ATTACCAAGG                               40
```


(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
TACAGTGGAT CCATGGTTAT TTCAAATAAT TTATAAAAGC AC                           42
```


(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCATTGGAT CCATGGTTAA CACACTAAGC AAGCAC   36

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCTAATCTA GAACCATGGA TGACTCACTA AGGAAAGCAT TGTTGC   46

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCCACTATCC TTCGCAAGAC CC   22

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACAGTGGAT CCATGGTTAA GGTAATCCAT AGGCTTGAC   39

(2) INFORMATION FOR SEQ ID NO:26:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 40 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGCTAACCAT GGTTAAGCTC ACTAAGGAAA GCATTGTTGC   40

(2) INFORMATION FOR SEQ ID NO:27:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 46 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCTAATCTA GAACCATGGA TGACTCACTA AGGAAAGCAT TGTTGC   46

(2) INFORMATION FOR SEQ ID NO:28:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 36 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCATTGGAT CCATGGTTAA CACACTAAGC AAGCAC   36

(2) INFORMATION FOR SEQ ID NO:29:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 39 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TACAGTTCTA GAACCATGGA TGATGCAAAG TCTGTGAGG   39

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 49 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGATTCTCTA GACCATGGTG ACTTGATGAG CAAAGTCTGT GAGGCTTGC   49